

REPLACEMENT SHEET



SEQ ID 2 1 ATG TTG CAG ATG GCT GGG CAG TGC TCC CAA AAT GAA TAT TTT GAC AGT TTG TTG CAT GCT
 SEQ ID 1 11 M L Q M A G Q C S Q N E Y F D S L L L H A
 61 TGC ATA CCT TGT CAA CTT OGA TGT TCT TCT AAT ACT CCT OCT CTA ACA TGT CAG CGT TAT
 211 C I P C Q L R C S S N T P P L T C Q R Y
 121 TGT AAT GCA AGT GTG ACC AAT TCA GTG AAA GGA ACG AAT GCG ATT CTC TGG ACC TGT TTG
 411 C N A S V T N S V K G T N A I L W T C L
 181 GGA CTG AGC TTA ATA ATT TCT TTG GCA GTT TTC GTG CTA ATG TTT TTG CTA AGG AAG ATA
 611 G L S L I I S L A V F V L M F L L R K I
 241 AGC TCT GAA OCA TTA AAG GAC GAG TTT AAA AAC ACA GGA TCA GGT CTC CTG GGC ATG GCT
 811 S S E P L K D E F K N T G S G L L G M A
 301 AAC ATT GAC CTG GAA AAG AGC AGG ACT GGT GAT GAA ATT ATT CTT OCG AGA GGC CTC GAG
 1011 N I D L E K S R T G D E I I L P R G L E
 361 TAC ACG GTG GAA GAA TGC ACC TGT GAA GAC TGC ATC AAG AGC AAA OCG AAG GTC GAC TCT
 1211 Y T V E E C T C E D C I K S K P K V D S
 421 GAC CAT TGC TTT OCA CTC OCA GCT ATG GAG GAA GGC GCA ACC ATT CTT GTC ACC ACG AAA
 1411 D H C F P L P A M E G A T I L V T T K
 481 ACG AAT GAC TAT TGC AAG AGC CTG OCA GCT GCT TTG AGT GCT ACG GAG ATA GAG AAA TCA
 1611 T N D Y C K S L P A A L S A T E I E K S
 541 ATT TCT GCT AGG TAA
 1811 I S A R .

FIG. 1

REPLACEMENT SHEET

SEQ ID NO:8

1 AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCGCGAAG
 61 ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG TTCATTGTTT TCAACATTCT
 121 AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC

181 TGTCTTTTCT GTAGCTCCCT TGTCTTCTTT TGTGATCAT GTTGCAGATG GCTGGGCAGT
 SEQ ID NO:1 1► M L Q M A G Q

241 GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT
 8► C S Q N E Y F D S L L H A C I P C Q L R

301 GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT
 28► C S S N T P P L T C Q R Y C N A S V T N

361 CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT
 48► S V K G T N A I L W T C L G L S L I I S
 421 TGGCAGTTT CGTGCTAATG TTTTGTCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG
 68► L A V F V L M F L L R K I S S E P L K D

481 AGTTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA
 88► E F K N T G S G L L G M A N I D L E K S

541 GGAAGTGGTA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
 108► R T G D E I I L P R G L E Y T V E E C T

601 GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG
 128► C E D C I K S K P K V D S D H C F P L P
 661 CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC
 148► A M E E G A T I L V T T K T N D Y C K S

721 TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA
 168► L P A A L S A T E I E K S I S A R

781 TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTGTGTCAG AATAGATGAT GTGTCAGATC
 841 TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCTCTT AACTGTGGAA

901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAAACTTC
 961 CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA

FIG. 3

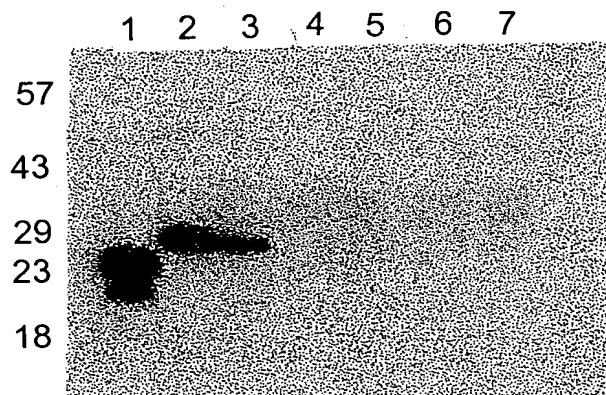


FIG. 7

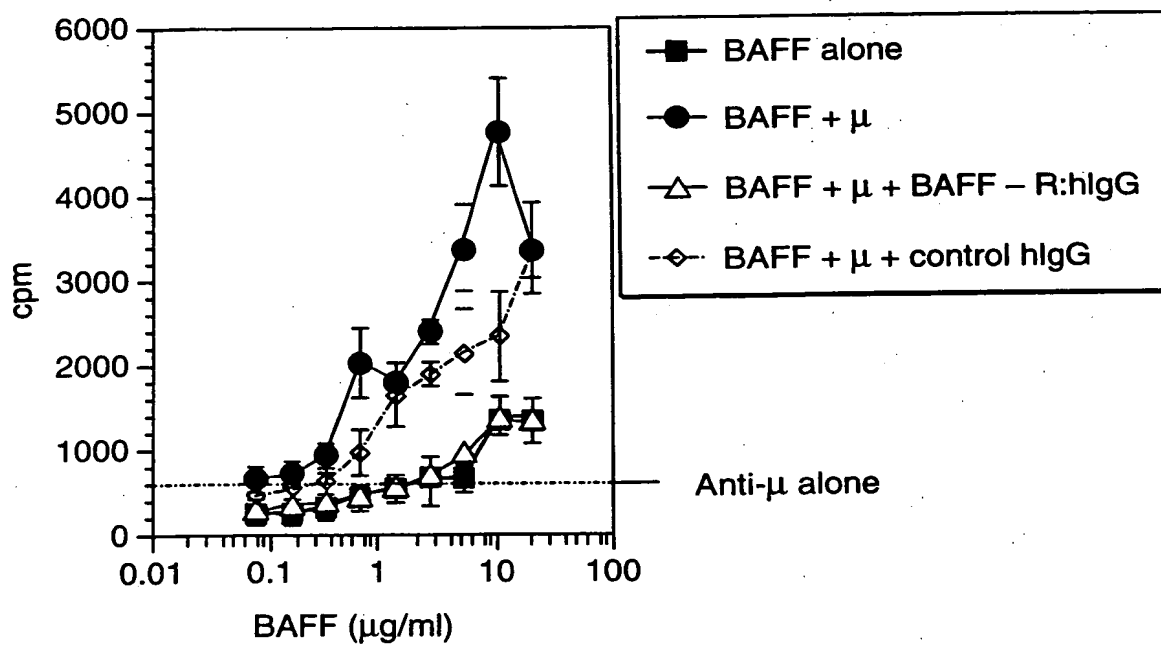


FIG. 8